

Listing of claims:

This listing of claims will replace all prior versions and listings of claims in the application. Please amend the application by amending claims 1, 3, 9-10, 18, 20, 25-26, 34-35, and 37-38; canceling claims 8, 24, and 36; and adding new claims 43-61 as indicated below.

1 1. (Currently Amended) A method for identifying oligonucleotide sequences
2 suitable for the amplification of a unique sequence within a genomic region of interest,
3 said method comprising the steps of:
4 executing a first process on a digital computer to identify repeat sequences
5 that occur within said genomic region of interest;
6 executing a second process on a digital computer to compare repeat
7 sequence-free subsequences within said genomic region of interest to a nucleotide
8 sequence database, whereby nucleotide sequences within said nucleotide sequence
9 database that are ~~substantially similar~~ at least 50% identical to said repeat sequence-free
10 subsequences are identified;
11 executing a third process on a digital computer to identify oligonucleotide
12 sequences that are suitable for use as primers in an amplification reaction to amplify a
13 product within at least one of said repeat sequence-free subsequences for which a ~~defined~~
14 ~~number of 5 or fewer~~ substantially similar sequences that are at least 50% identical are
15 identified in said nucleotide sequence database; and
16 outputting said oligonucleotide sequences.

1 2. (Original) The method of claim 1, wherein said genomic region is from a human
2 genome.

1 3. (Currently Amended) The method of claim 1, wherein ~~said defined number of~~
2 ~~substantially similar sequences is zero~~ the third process comprises identifying
3 oligonucleotide sequences that are suitable for use as primers in an amplification reaction

4 to amplify a product within at least one of said repeat sequence-free subsequences that
5 lacks any sequences that are at least 50% identical to said nucleotide sequence database.

1 4. (Original) The method of claim 1, wherein said oligonucleotide sequences are
2 outputted by displaying the sequences on a computer screen or on a computer printout.

1 5. (Original) The method of claim 1, wherein said oligonucleotide sequences are
2 outputted by executing a fourth process on a digital computer to direct the synthesis of
3 oligonucleotide primers comprising said oligonucleotide sequences.

1 6. (Original) The method of claim 5, wherein said computer directs the synthesis of
2 said oligonucleotide primers by ordering said synthesis from an external source.

1 7. (Original) The method of claim 5, wherein said computer is in communication
2 with an oligonucleotide synthesizer, and wherein said computer directs the synthesis of
3 said oligonucleotide primers by said synthesizer.

1 8. (Canceled)

1 9. (Currently Amended) The method of claim 1, wherein said 5 or fewer
2 ~~substantially similar~~ sequences are at least ~~about~~ 70% identical to said repeat sequence-
3 free subsequences.

1 10. (Currently Amended) The method of claim 1, wherein said 5 or fewer
2 ~~substantially similar~~ sequences are at least ~~about~~ 90% identical to said repeat sequence-
3 free subsequences.

1 11. (Previously Amended) The method of claim 1, wherein said first process is
2 executed using a software program that screens sequences for:

- 3 i. interspersed repeats that are known to exist in mammalian
4 genomes and;
5 ii. low complexity DNA sequences.

1 12. (Previously Amended) The method of claim 1, wherein said second process is
2 executed using a sequence comparison algorithm.

1 13. (Original) The method of claim 1, wherein said third process is executed using
2 Primer3 software.

1 14. (Original) The method of claim 5, further comprising producing an amplification
2 product using said oligonucleotide primers.

1 15. (Original) The method of claim 14, wherein said amplification product is a FISH
2 probe.

1 16. (Original) The method of claim 15, wherein said FISH probe is fluorescently
2 labeled.

1 17. (Original) The method of claim 14, wherein said amplification product is an array
2 CGH target.

1 18. (Currently Amended) A method for identifying oligonucleotide sequences
2 suitable for the amplification of a unique sequence within a genomic region of interest,
3 said method comprising the steps of:

4 analyzing a genomic nucleotide sequence that encompasses said genomic
5 region of interest to identify repeat sequences within said genomic region;

6 comparing at least one repeat sequence-free subsequence within said
7 genomic nucleotide sequence to a nucleotide sequence database to identify sequences
8 within said database that are ~~substantially similar~~ at least 50% identical to said repeat
9 sequence-free subsequence;

10 for at least one of said repeat sequence-free subsequences for which a
11 ~~defined number of 5 or fewer substantially similar~~ sequences that are at least 50%
12 identical are identified within said nucleotide sequence database, selecting
13 oligonucleotide sequences that are suitable for use as primers in an amplification reaction
14 to amplify a product within said repeat sequence-free subsequence.

1 19. (Original) The method of claim 18, wherein said genomic region is from a human
2 genome.

1 20. (Currently Amended) The method of claim 18, wherein said ~~defined number of~~
2 ~~substantially similar sequences is zero~~ oligonucleotide sequences that are suitable for use
3 as primers in an amplification reaction to amplify a product within said repeat sequence-
4 free subsequence are selected from at least one of said repeat sequence-free subsequences
5 that lack any sequences that are at least 50% identical to said nucleotide sequence
6 database.

1 21. (Original) The method of claim 18, further comprising displaying said
2 oligonucleotide sequences on a computer screen or on a computer printout.

1 22. (Original) The method of claim 18, further comprising directing the synthesis of
2 oligonucleotide primers comprising said oligonucleotide sequences.

1 23. (Original) The method of claim 22, wherein said synthesis is directed by ordering
2 the synthesis of said primers from an external source.

1 24. (Canceled)

1 25. (Currently Amended) The method of claim 18, wherein said 5 or fewer
2 ~~substantially similar~~ sequences are at least ~~about~~ 70% identical to said repeat sequence-
3 free subsequences.

1 26. (Currently Amended) The method of claim 18, wherein said 5 or fewer
2 ~~substantially similar~~ sequences are at least ~~about~~ 90% identical to said repeat sequence-
3 free subsequences.

1 27. (Previously Amended) The method of claim 18, wherein the identification of
2 repeat sequences within said genomic region is performed using a software program that
3 screens sequences for:

- 4 i. interspersed repeats that are known to exist in mammalian
5 genomes and;
6 ii. low complexity DNA sequences.

1 28. (Previously Amended) The method of claim 18, wherein the comparison of said at
2 least one repeat sequence-free subsequence with said genome database is performed
3 using a sequence comparison algorithm.

1 29. (Original) The method of claim 18, wherein said oligonucleotide sequences are
2 selected using Primer3 software.

1 30. (Original) The method of claim 22, further comprising generating an
2 amplification product using said oligonucleotide primers.

1 31. (Original) The method of claim 30, wherein said amplification product is a FISH
2 probe.

1 32. (Original) The method of claim 31, wherein said FISH probe is fluorescently
2 labeled.

1 33. (Original) The method of claim 30, wherein said amplification product is an array
2 CGH target.

1 34. (Currently Amended) A computer program product designing and outputting
2 oligonucleotide sequences suitable for use as primers to amplify unique sequences within
3 a genomic region of interest, said computer program product comprising:

4 a storage structure having computer program code embodied therein, said
5 computer program code comprising:

6 computer program code for causing a computer to analyze a nucleotide
7 sequence encompassing said genomic region of interest to identify repeat sequences
8 within said nucleotide sequence;

9 computer program code for causing a computer to, for each subsequence
10 of said nucleotide sequence that does not contain any of said repeat sequences, compare

11 said subsequence against a nucleotide sequence database to identify nucleotide sequences
12 within said database that are ~~substantially similar~~ at least 50% identical to said
13 subsequence;
14 computer program code for causing a computer to, for ~~each~~ at least one of
15 said subsequences for which a ~~defined number of 5 or fewer~~ substantially similar
16 sequences that are at least 50% identical are found in said database, identify
17 oligonucleotide sequences suitable for use as primers in an amplification reaction to
18 amplify a product within said subsequence; and
19 computer program code for outputting said oligonucleotide sequences.

1 35. (Currently Amended) The method of claim 34, wherein said ~~defined number of~~
2 ~~substantially similar sequences is zero~~ oligonucleotide sequences that are suitable for use
3 as primers in an amplification reaction to amplify a product within said subsequence are
4 identified from at least one of said subsequences that lack any sequences that are at least
5 50% identical to said database.

1 36. (Canceled)

1 37. (Currently Amended) The method of claim 34, wherein said 5 or fewer
2 ~~substantially similar~~ sequences are at least ~~about~~ 70% identical to said subsequences.

1 38. (Currently Amended) The method of claim 34, wherein said 5 or fewer
2 ~~substantially similar~~ sequences are at least ~~about~~ 90% identical to said subsequences.

1 39. (Canceled)

1 40. (Previously Added) The method of claim 1, wherein the repeat-free subsequences
2 are each at least 100 bp long.

1 41. (Previously Added) The method of claim 18, wherein the repeat-free
2 subsequences are each at least 100 bp long.

1 42. (Previously Added) The computer program of claim 34, wherein each nucleotide
2 sequence that does not contain any of the repeat sequences is at least 100 bp long.

1 ~~43.~~ (New) A method for identifying oligonucleotide sequences suitable for the
2 amplification of a unique sequence within a genomic region of interest, said method
3 comprising the steps of:
4 executing a first process on a digital computer to identify repeat sequences
5 that occur within said genomic region of interest;
6 executing a second process on a digital computer to compare repeat
7 sequence-free subsequences within said genomic region of interest to a nucleotide
8 sequence database, whereby at least one repeat sequence-free subsequences that is at least
9 90% identical to a nucleotide sequence within said nucleotide sequence database is
10 discarded;
11 executing a third process on a digital computer to identify oligonucleotide
12 sequences that are suitable for use as primers in an amplification reaction to amplify a
13 product within at least one repeat sequence-free subsequences remaining after executing
14 said second process; and
15 outputting said oligonucleotide sequences.

1 44. (New) The method of claim 43, wherein said genomic region is from a human
2 genome.

1 45. (New) The method of claim 43, wherein said oligonucleotide sequences are
2 outputted by displaying the sequences on a computer screen or on a computer printout.

1 46. (New) The method of claim 43, wherein said oligonucleotide sequences are
2 outputted by executing a fourth process on a digital computer to direct the synthesis of
3 oligonucleotide primers comprising said oligonucleotide sequences.

1 47. (New) The method of claim 43, wherein said computer directs the synthesis of
2 said oligonucleotide primers by ordering said synthesis from an external source.

1 48. (New) The method of claim 43, wherein said computer is in communication with
2 an oligonucleotide synthesizer, and wherein said computer directs the synthesis of said
3 oligonucleotide primers by said synthesizer.

1 49. (New) The method of claim 43, wherein all repeat sequence-free subsequences
2 that are at least 70% identical to a nucleotide sequence within said nucleotide sequence
3 database are discarded.

1 50. (New) The method of claim 43, wherein all repeat sequence-free subsequences
2 that are at least 50% identical to a nucleotide sequence within said nucleotide sequence
3 database are discarded.

1 51. (New) The method of claim 43, wherein said first process is executed using a
2 software program that screens sequences for:

- 3 i. interspersed repeats that are known to exist in mammalian
4 genomes and;
5 ii. low complexity DNA sequences.

1 52. (New) The method of claim 43, wherein said second process is executed using a
2 sequence comparison algorithm.

1 53. (New) The method of claim 43, wherein said third process is executed using
2 Primer3 software.

1 54. (New) The method of claim 43, further comprising producing an amplification
2 product using said oligonucleotide primers.

1 55. (New) The method of claim 43, wherein said amplification product is a FISH
2 probe.

1 56. (New) The method of claim 43, wherein said FISH probe is fluorescently labeled.

1 57. (New) The method of claim 43, wherein said amplification product is an array
2 CGH target.

1 58. (New) The method of claim 43, wherein the repeat-free subsequences are each at
2 least 100 bp long.

1 59. (New) The method of claim 43, wherein all repeat sequence-free subsequences
2 that are at least 90% identical to a nucleotide sequence within said nucleotide sequence
3 database are discarded.

1 ~~60.~~ (New) A method for identifying oligonucleotide sequences suitable for the
2 amplification of a unique sequence within a genomic region of interest, said method
3 comprising the steps of:

4 (1) analyzing a genomic nucleotide sequence that encompasses said
5 genomic region of interest to identify repeat sequences within said genomic region;

6 (2) comparing repeat sequence-free subsequences within said genomic
7 region of interest to a nucleotide sequence database, whereby at least one repeat
8 sequence-free subsequences that is at least 90% identical to a nucleotide sequence within
9 said nucleotide sequence database is discarded;

10 (3) identifying oligonucleotide sequences that are suitable for use as
11 primers in an amplification reaction to amplify a product within at least one repeat
12 sequence-free subsequences remaining after step (2).

1 ~~61.~~ (New) A computer program product designing and outputting oligonucleotide
2 sequences suitable for use as primers to amplify unique sequences within a genomic
3 region of interest, said computer program product comprising a storage structure having
4 computer program code embodied therein, said computer program code comprising the
5 elements:

6 (1) computer program code for causing a computer to analyze a nucleotide
7 sequence encompassing said genomic region of interest to identify repeat sequences
8 within said nucleotide sequence;